

1001 GTCAACACTA CTGTTGCCCTT AAGCTGCACC TGCCGAGGCA GCGGCAACCT ACAGGACGAG TGTGAACAGC TGGAAAAGGTC CTTCTCCAG AACCCCTGCC
 CAGTTGTGAT GACAACGGAA TTCGACGTGG ACGGCTCCGT CGCGTTGGA TGCTGCTC ACCTTTCCAG GAAGGGTC TTGGGGACGG
 305 ValAsnThrT hrValAlaLe userCysThr CysArgGlys erGlyAsnLe uGlnAspGlu CysGluGlnL euGluArgSe rPheSerGln AsnProCysLeu
 1101 TCGTGGAGGC CATTGCAGCT AAGATGCGTT TCCACAGACA GCTCTTCTCC CAGGACTGGG CAGACTCTAC TTTTTCAGTG GTGCAGCAGC AGAACAGCAA
 AGCACCTCCG GTAACGTGCGA TTCTACCGAA AGGTGCTGTG CGAGAAGAGG GTCCTGACCC GTCTGAGATG AAAAAGTCAC CACGCTGCTCG TCTTGTCTGT
 339 ValGluAl aileAlaAla LysMetArgP heHisArgG1 nLeuPheSer GlnAspTrpA laAspSerVal ValGlnGlnG InAsnSerAsn
 1201 CCCTGCTCTG AACTGCAGC CCAGGCTACC CATTCTTTCT TTCTCCATCC TTCCCTTGAT TCTGCTGAG ACCCTCTGGT AGCTGGGCTT CCTCAGGGTC
 GGGACGAGAC TCTGACGTG GGTCCGATGG GTAAGAAAGA AAGAGGTAGG AAGGGAATA AGACGACGTC TGGGAGACCA TCGACCCGAA GGAGTCCCAG
 372 ProAlaLeu ArgLeuGlnP roArgLeuPr oileLeuSer PheSerIleL euProLeuI ThrLeuTrp
 1301 CTTTGTCTC TCCACCACAC CCAGACTGAT TTGCAGCCTG TGGTGGGAGA GAACTCGCA GCCTGTGGA GAAGACGCAG CGTGTCTACAC AGCAACCCCG
 GAAACAGGAG AGGTGGTGTG GGTCTGACTA AACGTCGGAC ACCACCTCT CTTGAGCGGT CGGACACCTT CTTCTGCGTC GCACGATGTG TCGTTGGGCC
 1401 AACCAACCAG GCATTCCGCA GCACATCCCG TCTGCTCCAG AAGAGTCTT AGAAGTGAGG GCTGTGACCC TTCCGATCCT GAGCGGCTAG TTTTCAAAAC
 TTGGTTGCTC CGTAAGCGT CGTGTAGGC AGACGAGGTC TTCTCCAGAA TCTTCACTCC CGACACTGGG AAGGCTAGGA CTCGCCGATC AAAAGTTTGG
 1501 TCCCTTGCCC CTGCTTCTCT CTGGCTCAGG CTGCTCCTCC TTAGGACTTT GTGGGTCCAG TTTTGCCTTC TGTCTGTATG GTGATTAGCG GCTCACCTCC
 AGGGAACGGG GACGAAGGAA GACCGAGTCC GACGAGGAGG AATCTGAAA CACCCAGGTC AAAACGGAG ACAAGACTAC CACTAATCGC CGAGTGGAGG
 1601 AGCGCTTCTT CCTGTTTCCC AGGACCACCC AGAGGCTAAG GAATCAGTCA TTCCCTCTTG CTTCTCTCCAG GAAGGCAGGC TAAGGGTTCT GAGGTGACTG
 TCGCGAAGAA GGACAAAGG TCCTGGTGGG TCCTCCGATT CTTAGTCAGT AAGGGACAAC GGAAGAGGTC CTTCCGTCCG ATTCCCAGA CTCCACTGAC
 1701 AGAAAAATGT TTCCTTTGTG TGAAGGCTG GTGCTCCAGC CTCACGTCCT CTCTGAATGG AAGATAAAA CCTGCTGGTG TCTTGACTGC TCTGCCAGGC
 TCTTTTACA AAGGAAACAC ACCTTCCGAC CACGAGGTG CAGGTGCAGG GAGACTTACC TTCTATTTT GGACGACCAC AGAACTGACG AGACGGTCCG
 1801 AATCCTGAAC ATTTGGGCAT GAAGAGCTAA AGTCTTTGGG TCTTGTTTAA CTCCTATTAC TGTCCCCAAA TTCCCCCTAGT CCCTTGGGTC ATGATTAAAC
 TTAGGACTTG TAAACCCGTA CTTCTCGATT TCAGAAACCC AGAACAAATT GAGGATATG ACAGGGGTTT AAGGGGATCA GGAACCCAG TACTAATTG
 1901 ATTTTGACTT AAAAAAAA AAAAAAAA AAAAAA
 TAAACTGAA TTTTTTTTTT TTTTTTTTTT TTTTTT

FIG. 1B

hGFra3	1	M	V	R	P	L	N	P	R	P	L	P	P	V	V	L	M	L	L	L	L	L	L	P	P	S	P	L	P	L	A	A	G	D	P	L	P	T	E	S	R	L	M	N	S	C	L	Q	A	R	R	K
mGFra3	1	.	.	.	M	G	L	S	W	S	P	R	P	P	L	L	M	I	L	L	L	V	L	S	L	W	.	L	P	L	G	A	G	N	S	L	A	T	E	N	R	F	V	N	S	C	T	Q	A	R	K	

hGFra3	51	C	Q	A	D	P	T	C	S	A	A	Y	H	L	D	S	C	T	S	S	I	S	T	P	L	P	S	E	E	P	S	V	P	A	D	C	L	E	A	A	Q	L	R	N	S	S	L	I	G		
mGFra3	48	C	E	A	N	P	A	C	K	A	A	Y	Q	H	L	G	S	C	T	S	S	L	S	R	P	L	P	L	E	E	S	A	M	S	A	D	C	L	E	A	A	E	Q	L	R	N	S	S	L	I	D

hGFra3	101	C	M	C	H	R	R	M	K	N	Q	V	A	C	L	D	I	Y	W	T	V	H	R	A	R	S	L	G	N	Y	E	L	D	V	S	P	Y	E	D	T	V	T	S	K	P	W	K	M	N	L	S
mGFra3	98	C	R	C	H	R	R	M	K	H	Q	A	T	C	L	D	I	Y	W	T	V	H	P	A	R	S	L	G	D	Y	E	L	D	V	S	P	Y	E	D	T	V	T	S	K	P	W	K	M	N	L	S

hGFra3	151	K	L	N	M	L	K	P	D	S	D	L	C	L	K	F	A	M	L	C	T	L	N	D	K	C	D	R	L	R	K	A	Y	G	E	A	C	S	G	P	H	C	Q	R	H	V	C	L	R	Q	L
mGFra3	148	K	L	N	M	L	K	P	D	S	D	L	C	L	K	F	A	M	L	C	T	L	H	D	K	C	D	R	L	R	K	A	Y	G	E	A	C	S	G	I	R	C	Q	R	H	L	C	L	A	Q	L

hGFra3	201	L	T	F	F	E	K	A	A	E	P	H	A	Q	G	L	L	L	C	P	C	A	P	N	D	R	G	C	G	E	R	R	R	N	T	I	A	P	N	C	A	L	P	P	V	A	P	N	C	L	E
mGFra3	198	R	S	F	F	E	K	A	A	E	S	H	A	Q	G	L	L	L	C	P	C	A	P	E	D	A	G	C	G	E	R	R	R	N	T	I	A	P	S	C	A	L	P	S	V	T	P	N	C	L	D

hGFra3	251	L	R	R	L	C	F	S	D	P	L	C	R	S	R	L	V	D	F	Q	T	H	C	H	P	M	D	I	L	G	T	C	A	T	E	Q	S	R	C	L	R	A	Y	L	G	L	I	G	T	A	M
mGFra3	248	L	R	S	F	C	R	A	D	P	L	C	R	S	R	L	M	D	F	Q	T	H	C	H	P	M	D	I	L	G	T	C	A	T	E	Q	S	R	C	L	R	A	Y	L	G	L	I	G	T	A	M

hGFra3	301	T	P	N	F	V	S	N	V	N	T	S	V	A	L	S	C	T	C	R	G	S	G	N	L	Q	E	E	C	E	M	L	E	G	F	F	S	H	N	P	C	L	T	E	A	I	A	A	K	M	R
mGFra3	298	T	P	N	F	I	S	K	V	N	T	T	V	A	L	S	C	T	C	R	G	S	G	N	L	Q	D	E	C	E	Q	L	E	R	S	F	S	Q	N	P	C	L	V	E	A	I	A	A	K	M	R

hGFra3	351	F	H	S	Q	L	F	S	Q	D	W	P	H	P	T	F	A	V	M	A	H	Q	N	E	N	P	A	V	R	P	Q	P	W	V	P	S	L	F	S	C	T	L	P	L	L	L	S	L	W
mGFra3	348	F	H	R	Q	L	F	S	Q	D	W	A	D	S	T	F	S	V	V	Q	Q	N	S	N	P	A	L	R	L	Q	P	R	L	P	I	L	S	F	S	I	L	P	L	L	Q	T	L	W	

FIG. 3

48613 1 MVRPLNPRPLPPVVLMLLLLLPPSPPLPLAAGDPLPTESRLMNSCLQARRK
48614 1 MVRPLNPRPLPPVVLMLLLLLPPSPPLPLAAGDPLPTESRLMNSCLQARRK

48613 51 CQADPTCSAAYHHLDSDCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG
48614 51 CQADPTCSAAYHHLDSDCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG

48613 101 CMCHRRMKKNQVACLDIYWTVHRARSLGNYELDVSPYEDT VTSKPWKMNLS
48614 101 CMCHRRMKKNQVACLDIYWTVHRARSL

48613 151 KLNMLKPPDSDLCLKFAMLCTLNDKCDRLRKAYGEACSGPHCVCLRQL
48614 127 DSDLCLKFAMLCTLNDKCDRLRKAYGEACSGPHCVCLRQL

48613 201 LTFEKEAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE
48614 170 LTFEKEAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE

48613 251 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM
48614 220 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM

48613 301 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR
48614 270 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR

48613 351 FHSQLFSQDWPHPPTFAVMAHQENENPAVRPQPWPVPSLFSCTLPLILLLSLW
48614 320 FHSQLFSQDWPHPPTFAVMAHQENENPAVRPQPWPVPSLFSCTLPLILLLSLW

FIG. 4

DNA48613.orf 1 A T G G T G C G C C C C C T G A A C C G C G A C C G C T G C C G C C C G T A G T C T G A T G T T
GENFRa1.orf 1 A T G A T C T T G G C A A A C G T C T T C T G C T C T T C T T C T T C T T
GENFRa2.orf 1 A T G A T C T T G G C A A A C G T C T T C T G C T C T T C T T C T T C T T

DNA48613.orf 51 G C T G C T G C T G C T G C C G C T G C C C G C T G C C T C T C G C A G C C G G A G A C C C C C
GENFRa1.orf 6 C C T G G C G A C C C T G T A C T T C G C G C T G C C G C T C T T G G A C T T G C T C C T G T C G G
GENFRa2.orf 39 A G A C G A G A C C C T C G C T C T T T G G C C A G C C C T T C T C C T G C A G G C C C C G

DNA48613.orf 101 T T C C A C A G A A G C C G A C T C A T G A A C A G C T G T C T C C A G G C C A G G A G A G
GENFRa1.orf 56 C C G A A G T G A G C G G G A G A C C G C C T G G A T T G C G T G A A G C C A G T G A T C A G
GENFRa2.orf 89 A G C T C A C G G C T G G C G C C C C A G T G G A C T G T C C G G G C C A A T G A G C T G

DNA48613.orf 151 T G C C A G G C T G A T C C C A C C T G C A G T G C T G C C T A C C A C C A C T G G A T T C C T G
GENFRa1.orf 106 T G C C T G A A G A G C A G A G C T G C A G C A C C A A G T A C C G C A C G C T A A G G C A G T G
GENFRa2.orf 139 T G T G C C G C C G A T C C A A C T G C A G C T C T C G C T A C C G C A C T C T G C G G C A G T G

DNA48613.orf 201 C A C C T C T A G C A T A A G C A C C C C A C T G C C C T . . . C A G A G A G C C T T C G G T C C
GENFRa1.orf 156 C G T G C C G G C A A G G A G A C C A A C T T C A G C C T G G C A T C C G G C C T G G A G G C C A
GENFRa2.orf 189 C C T G G C A G G C C G C G A C C G C A C A C C A T G C T G G C C A

DNA48613.orf 248 C T G C T G A C T G C C T G G A G G C A G C A G C A C T C A G G A C A G C T C T G A T A
GENFRa1.orf 206 A G A T G A T G C C G C A G C G C C A T G G A G G C C C T G A A G C A G A G T C G C T C T A C
GENFRa2.orf 224 A C A G G A G T G C C A G G C G G C C T T G G A G G T C T T G C A G G A G A G C C C G C T G T A C

DNA48613.orf 298 G G C T G C A T G T G C C A C C G G C G C A T G A A G A A C C A G G T T G C C T G C T G G A C A T
GENFRa1.orf 256 A C T G C C G C T G C A A G C G G G T A T G A A G A A G G A A A G A A C T G C C T G C G C A T
GENFRa2.orf 274 G A C T G C C G C T G C A A G C G G G G C A T G A A G A A G G A G C T G C A G T G T C T G C A G A T

DNA48613.orf 348 C T A T T G G A C C G T T C A C C G T G C C C G C A G C C T T G G T A A C T A T G A G C T G G A T G
GENFRa1.orf 306 T T A C T G G A G C A T G T A C C A G A C C C T G C A G G G A A A T G A T C T G T G G A G G A T T
GENFRa2.orf 324 C T A C T G G A G C A T C A C C T G G G G C T G A C C G A G G T G A G G A G T T C T A C G A G

FIG. 5A

INA48613.orf 398 TCTCCCCCTATGAAG.....ACACAGTGAAGCAGC
 GDNFRa1.orf 356 CC[C]ATATGAACCAAGTTA.....ACAGCAGATTGTCA
 GDNFRa2.orf 374 CCTCCCCCTATGAGCCGGTGACCTCCGCTCTCGGACATCTTCAAGCTT

INA48613.orf 427 AAACCTGGAAATGAATCTCAGCAAACTGAACAATGCTCAACCAAGACTC
 GDNFRa1.orf 388 GATATATTCGGGTGGTCCCATTCATATCAGTGGAGCAATTCCCAAAGG
 GDNFRa2.orf 424 GCTTCAATCTTCTCAGGGACAAGGGCAAGACCCGGTGGTCAAGCCCAAGAG

INA48613.orf 477 AGACCTCTGCCTCAAGTTTGGCAATGCTGTGTACTCTCAATGACAAAGTGTG
 GDNFRa1.orf 438 GAAACAACCTGCCTGGATGCAAGCGAAGGCCCTGCAACCTCGACGACATTTGCA
 GDNFRa2.orf 474 CAACCATTGCCTGGATGCTGCCAAGGCCCTGCAACCTGAAATGACAACTGCA

INA48613.orf 527 ACCGGCTGCGCAAGGCCCTACGGGGAGGCGTGGCTCCGGGCCCACTG...C
 GDNFRa1.orf 488 AGAAGTACAAGTCCGGCTACATCAACCCTGCAACCAAGCTGTCT...C
 GDNFRa2.orf 524 AGAAGCTGCGCTCTCTACATCTCCATCTGCAACCGCGAGATCTCGCC

INA48613.orf 574 CAGGCGCAGCTCTGCTCAGGCAAGCTGCTCACTTTCTTCGAGAGGCGCGC
 GDNFRa1.orf 535 AATGATGTCTGCAACCGCCGCAAGTGCCACAAGGCCCTCCGGCAGTTCTT
 GDNFRa2.orf 574 ACCGAGCGCTGCAACCGCCGCAAGTGCCACAAGGCCCTGCGCAGTTCTT

INA48613.orf 624 CAGG.....CCCAACGCGCAGGCGCTGCTACTGTGCCATGTGCCCA
 GDNFRa1.orf 585 TGACAAAGGTCCGGCCAGACACAGCTACGGAAATGCTCTTCTGCTCCTGCC
 GDNFRa2.orf 624 CGACCGGGTGCCCAAGCGAGTACAACCTACCGCAATGCTCTTCTGCTCCTGCC

INA48613.orf 668 ACGACCGGGGCTGCGGGGAGCGCCCGGCGCAACACCATCGCCCAACTGC
 GDNFRa1.orf 635 GGGACATCGCCTGCAACAGAGCGGAGCGGCAACCATCGTGTGTGC
 GDNFRa2.orf 674 AAGACCAAGCGGTGCGCTGAGCGCCCGCGGCAACCATCTCTGCCCAAGCTGC

FIG. 5B

DNA48613.orf 718 GC GCTGCC...GCCTGTGGCCCCCAACTGCCCTGGAGCTGGGGCGCTCTG

GENFRa1.orf 585 T.CCTATGAAGAGAGGGAGAGGCCCAACTGTTGAAATTTGCAAGGACTCCTG

GENFRa2.orf 724 T.CCTATGAAGGACAAGGAGAGGCCCAACTGCCCTGGACCTGCGTGGCGTGTG

DNA48613.orf 765 CT TCTC GACCCGCTTTGGCAGATCAGGCCCTGGTGGATTTCCAGACCCACT

GENFRa1.orf 735 CAA GACGAA TTA CATCTGCAGATCTCGCCCTTGGCGATTTT TACCAACT

GENFRa2.orf 774 CCGGACTGACCACTGTGTGGTCCCGCTGGCCGACTTCCATGCCAATT

DNA48613.orf 815 GCCATCCCATGGACATCCTAGGAACCTTGTGCAACAGAGCAAGTCCAGA...

GENFRa1.orf 785 GCCAGCCAGAGTCAAGTCTGTCAAGCAGCTGTCTAAAGGA AACTACGCT

GENFRa2.orf 824 GTCGAGCCCTCCTACCAAGACGGTCAACAGCTGCCCTGCGGACAATTACCAAG

DNA48613.orf 862 ...TGCTACGAGCAATACCTGGGGCTGATTGGGACTGCCATGACCCCAA

GENFRa1.orf 835 GACTGCCTCTCGCCCTACTCGGGGCTTATTGGCACAAGTCA TGACCCCAA

GENFRa2.orf 874 GCGTGTCTGGCTCTTATGCTGGCATGATTGGGTTTGA CATGACACCTAA

DNA48613.orf 909 CTTTGTCA GCAATGTCA...ACACAGTGTG CCTTAAAGCTGCACT

GENFRa1.orf 885 CTACATAGACTCCAGTA...G CCTCAGTGTGGCCCATGGTGTGACT

GENFRa2.orf 924 CTATGTGGACTCCAAGCCCACTGGCATCGTGTGTCCCCCTGGTGCA GCT

DNA48613.orf 953 GCCGAGGCGAGTGGCAACCTG CAGGAGGAGTGTGAATGCTGGAAAGGTTT

GENFRa1.orf 929 GCA GCA CAGTGGGAACGACCTAGAAAGAGTGCTTGAATCTTGAATTTT

GENFRa2.orf 974 GTCGTGGCAGCGGGGAACATGGAGGAGGAGTGTGAGAAAGTCTCAGGGGAC

DNA48613.orf 1003 TTC TCCCAACAACCCCTTGCCTCACGGA GGCCATTGCAGCTAAGATGCGTTT

GENFRa1.orf 979 TTC AAGGACAATACATGTCTTAA AATGCAATTCAAGCCTTTGGCAATGG

GENFRa2.orf 1024 TTC ACCGAGAACCCATGCCTCCGGAACGCCATCCAGGCCCTTTGGCAACGG

FIG. 5C

DNA48613.orf 1053 T C A C A G C C A A C T C T T C T C C C A G G A C T G G C C A C A C C C T A C C T T T G C T G T G A
 GDNFRa1.orf 1029 C T C C G A T G T G A C C G T G T G G C A G C C A G C T T C C C A G T A C A G A C C A C C A C T G
 GDNFRa2.orf 1074 C A C G A C G T G A A C G T G T C C C A A A G G C C C C T C G T T C C A G G C C A C C C A G G

 DNA48613.orf 1103 T G G C A C A C C A G A T G A A A A C C C T G C T G T G A G G C C A C A G C C T G G G T G C C C
 GDNFRa1.orf 1079 C C A C T A C C A C C A C T G C C C T C G G G T T A A G A A C A A C C C T G G G C C A G C A
 GDNFRa2.orf 1124 C C C C T G G G T G G A G A G A C G C C T T C T T T G C C A G A T G A C C T C A G T G A C A G T

 DNA48613.orf 1153 T C T C T T T C T C C T G C A C G C T T C C C T T G A T T C T G C T C C T G A G C C T A T G G T A
 GDNFRa1.orf 1129 G G G T C T G A G A A T G A A A T T C C A C T C A T G T T T G C C A C C G T G T G C A A A T T T
 GDNFRa2.orf 1174 A C C A G C T T G G G G A C C A G T G T C A T C A C C A C C T G C A C G T C T G T C C A G G A G C A

 DNA48613.orf 1203 G
 GDNFRa1.orf 1179 A C A G G C A C A G A A G C T G A A A T C C A A T G T G T C G G G G C A A T A C A C A C C T C T G T A
 GDNFRa2.orf 1224 G G G G C T G A A G G C C A A C A A C T C C A A A G A G T T A A G C A T G T G C T T C A C A G A G C

 GDNFRa1.orf 1229 T T T C C A A T G G T A A T T A T G A A A A G A A G G T C T C G T G C T T C C A G C C A C A T A
 GDNFRa2.orf 1274 T C A C G A C A A A T A T C A T C C C A G G G A G T A A C A A G G T G A T C A A A C C T A A C T C A

 GDNFRa1.orf 1279 A C C A C A A A T C A A T G G C T G C T C T C A A G C T G T G G T C T G A G C C C A C T G C T
 GDNFRa2.orf 1324 G G C C C A G C A G A G C C A G A C C G T C G G C T G C C T T G A C C G T G C T G T C T G T C C T

 GDNFRa1.orf 1329 G G T C C T G G T G T A A C C G C T C T G T C C A C C C T A T T A T C T T T A C A G A A A C A T
 GDNFRa2.orf 1374 G A T G C T G A A C A G G C C T T G T A G

 GDNFRa1.orf 1379 C A T A G

FIG. 5D

DNA48613 1 M V R P L N P R P L P P V V L M L L L L P P S P L P L A A G D P L P T E S R L M N S C L Q A R R K
GDNFRa1 1 M F L A T . . . L Y F A L . . P L L D L L L S A . . E V S G G D R L . . D C V K A S D Q
GDNFRa2 1 M I L A N V F C L F F F L D E T L R S L A S P S . . S L Q G P E L H G W R P P V . . D C V R A N E L

DNA48613 51 C Q A D P T C S A A Y H H L D S C T S S I S T P L P . S E E P S V P A D C L E A A Q Q L R N S S L I
GDNFRa1 36 C L K E Q S C S T K Y R T L R Q C V A G K E T N F S L A S G L E A K D E C R S A M E A L K K K S L Y
GDNFRa2 47 C A A E S N C S S R Y R T L R Q C L A G R D R N T M L A N K E C Q A A L E V L Q E S P L Y

DNA48613 100 G C M C H R R M K N Q V A C L D I Y W T V H R A R S L G N Y E L D V S P Y E D T V T S K P W K M N L
GDNFRa1 86 N C R C K R G M K K E K N C L R I Y W S M Y Q S L . Q G N D L L E D S P Y E P V N S R L S D I F R V
GDNFRa2 92 D C R C K R G M K K E L Q C L Q I Y W S I H L G L T E G E E F Y E A S P Y E P V T S R L S D I F R L

DNA48613 150 S K L N M L K P D S D L C L K F A M L C T L N D K C D R L R K A Y G E A C S
GDNFRa1 135 V P F I S . . . V E H I . . P K G N N C L D A A K A C N L D D I C K K Y R S A Y I T P C T T S V S .
GDNFRa2 142 A S I F S G T G A D P V V S A K S N H C L D A A K A C N L N D N C K K L R S S Y I S I C N R E I S P

DNA48613 188 G P H C Q R H V C L R Q L L T F F E K A A E P H A Q G L L L C P C A P N D R G C G E R R R N T I A P
GDNFRa1 179 N D V C N R R K C H K A L R Q F F D K V P A K H S Y G M L F C S C . . R O I A C T E R R R Q T I V P
GDNFRa2 192 T E R C N R R K C H K A L R Q F F D R V P S E Y T Y R M L F C S C . . Q D Q A C A E R R R Q T I L P

DNA48613 238 N C A L P P V A . P N C L E L R R L C F S D P L C R S R L V D F Q T H C H P . M D I L G T C A T E Q
GDNFRa1 227 V C S Y E E R E K P N C L N L Q D S C K T N Y I C R S R L A D F F T N C Q P E S R S V S S C L K E N
GDNFRa2 240 S C S Y E D K E K P N C L D L R G V C R T D H L C R S R L A D F H A N C R A S Y Q T V T S C P A D N

DNA48613 286 . S R C L R A Y L G L I G T A M T P N F V S N V . . N T S V A L S C T C R G S G N L Q E E C E M L E
GDNFRa1 277 Y A D C L L A Y S G L I G T V M T P N Y I D S S . . S L S V A P W C D C S N S G N D L E E C L K F L
GDNFRa2 290 Y Q A C L G S Y A G M I G F D M T P N Y V D S S P T G I V V S P W C S C R G S G N M E E E C E K F L

DNA48613 333 G F F S H N P C L T E A I A A K M R F H S Q L F S
GDNFRa1 325 N F F K D N T C L K N A I Q A F G N G S D V T V W Q P A F P V Q T T A T T T T A L R V K N K P L G
GDNFRa2 340 R D F T E N P C L R N A I Q A F G N G T D V N V S P K G P S F Q A T Q A P R V E K T P S L P D D L S

DNA48613 358 Q D W P H P T F A V M A H Q N E N P A V R P Q
GDNFRa1 375 P A G S E N E I P T H V L P P C A N L Q A Q K L K S N V S G N T H L C I S N G N Y E K E G L G A S S
GDNFRa2 390 D S T S . . . L G T S V I T T C T S V Q E Q G L K A N N S K E L S M C F T . . E L T T N I I P G S N

DNA48613 381 P W V P S L F S C T L P L I L L L S L W
GDNFRa1 425 H I T T K S M A A P P S C G L S P L L V L V V T A L S T L L S L T E T S
GDNFRa2 435 K V I K P N S G P S R A R P S A A L T V L S V L M L K Q A L

FIG. 6

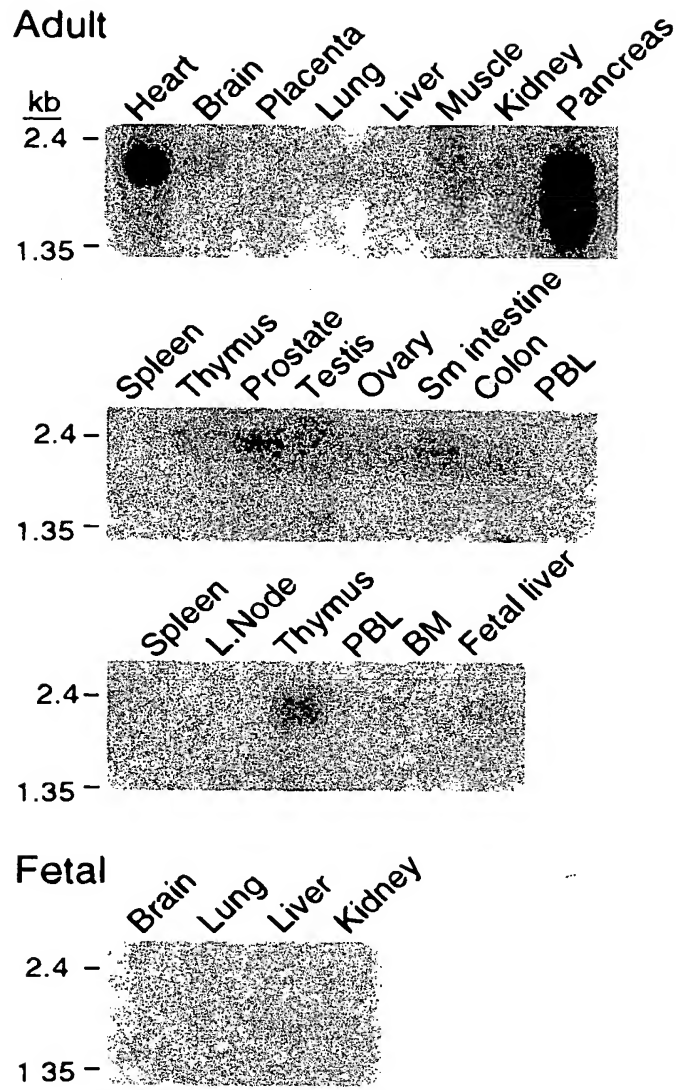


FIG. 7

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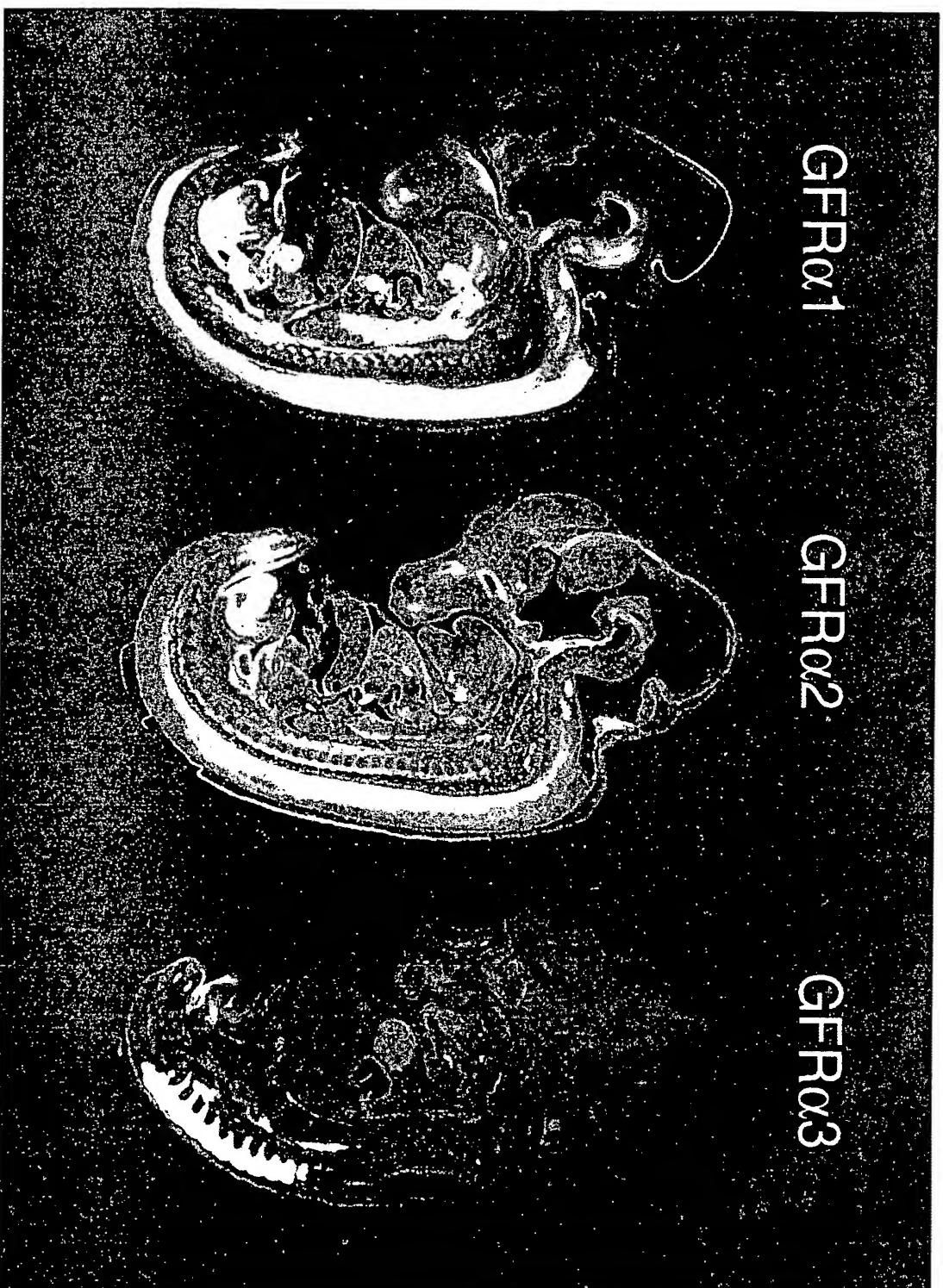
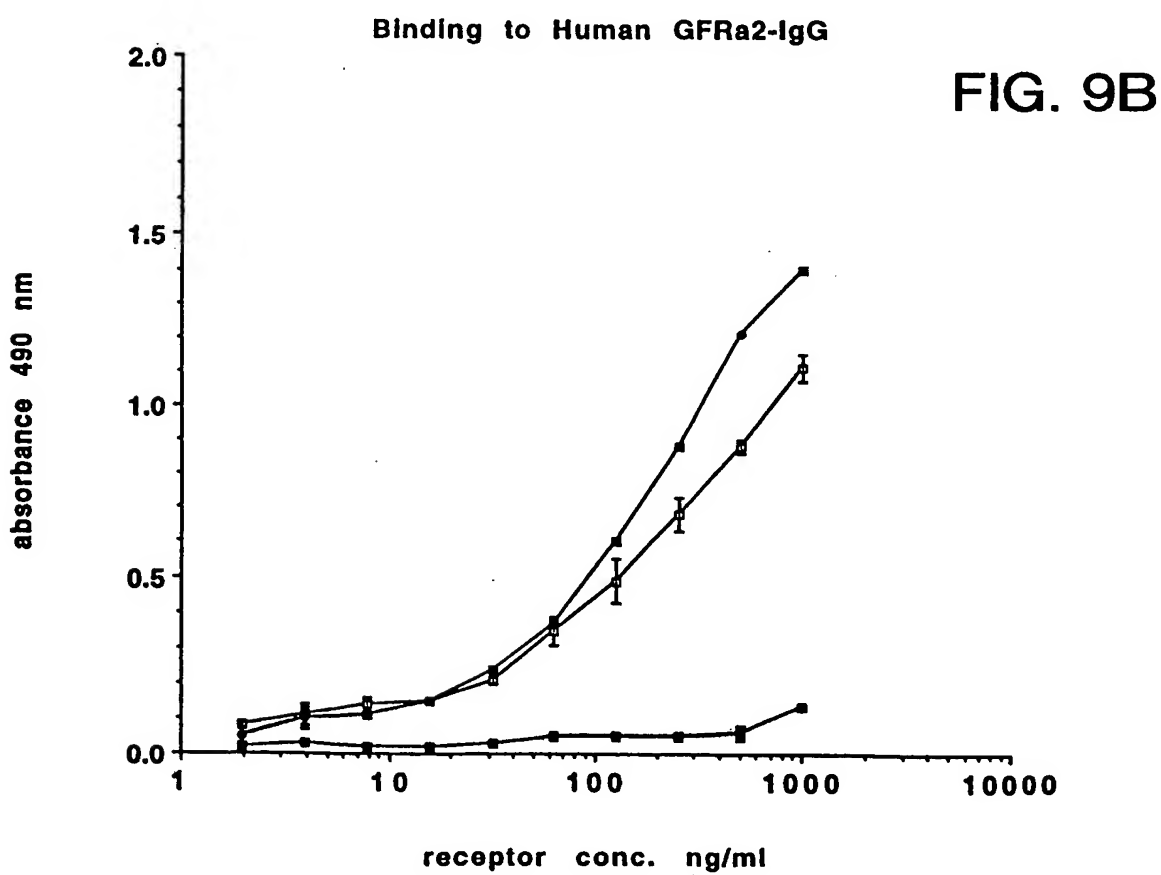
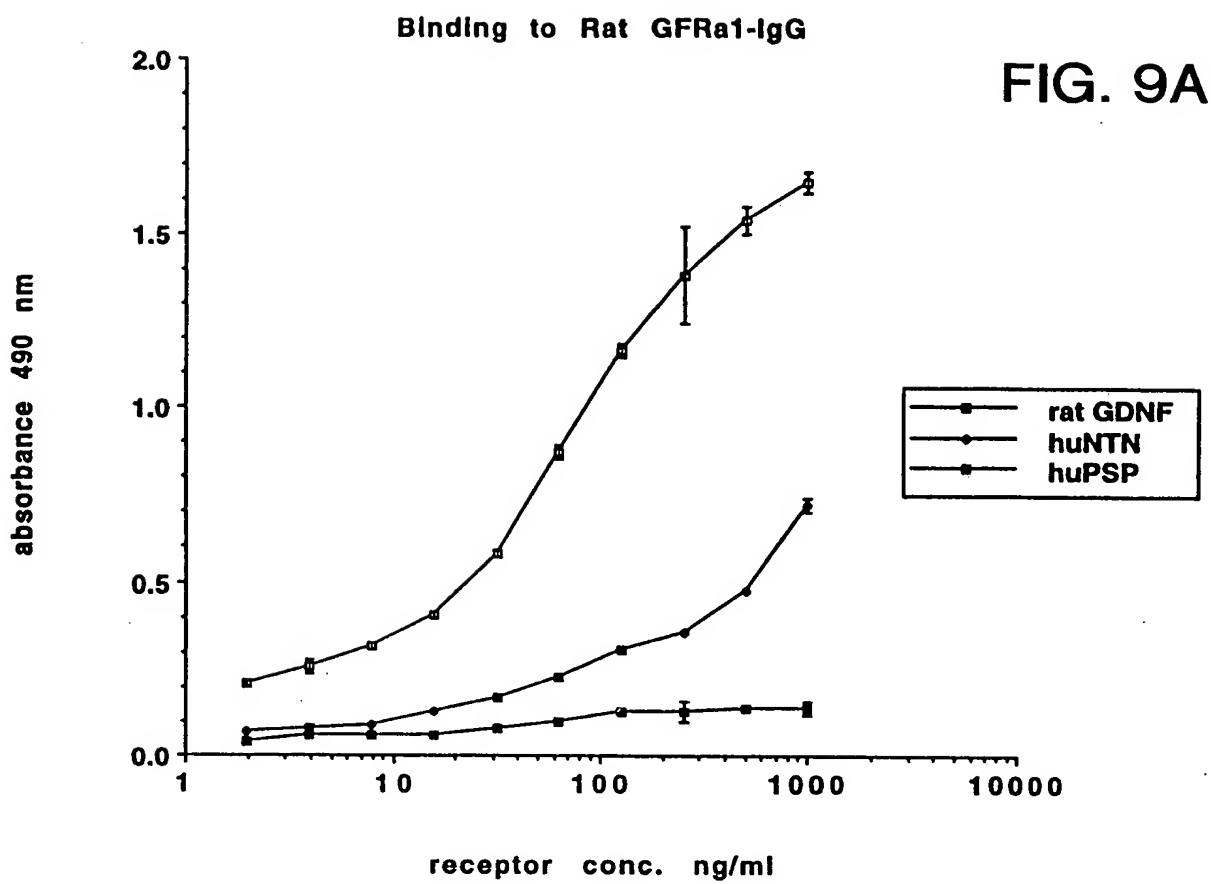


FIG. 8



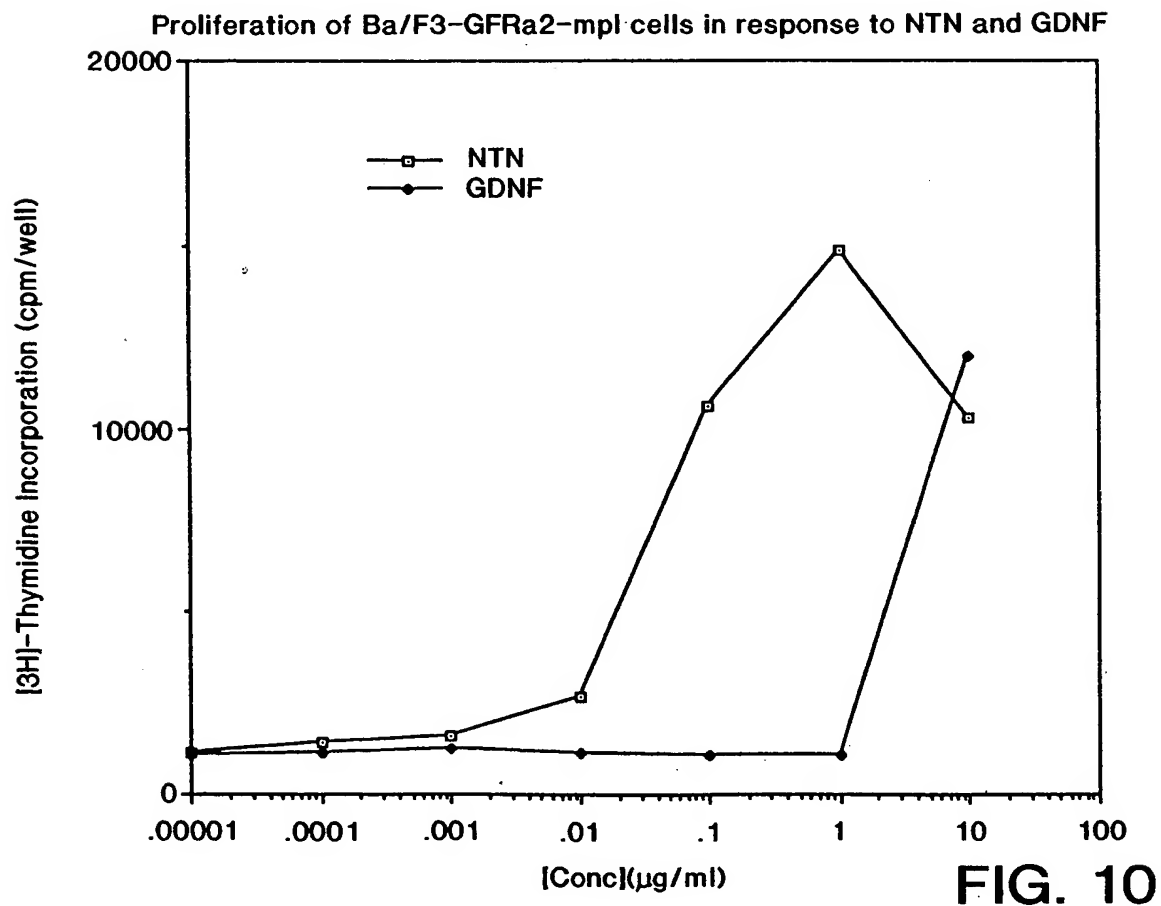
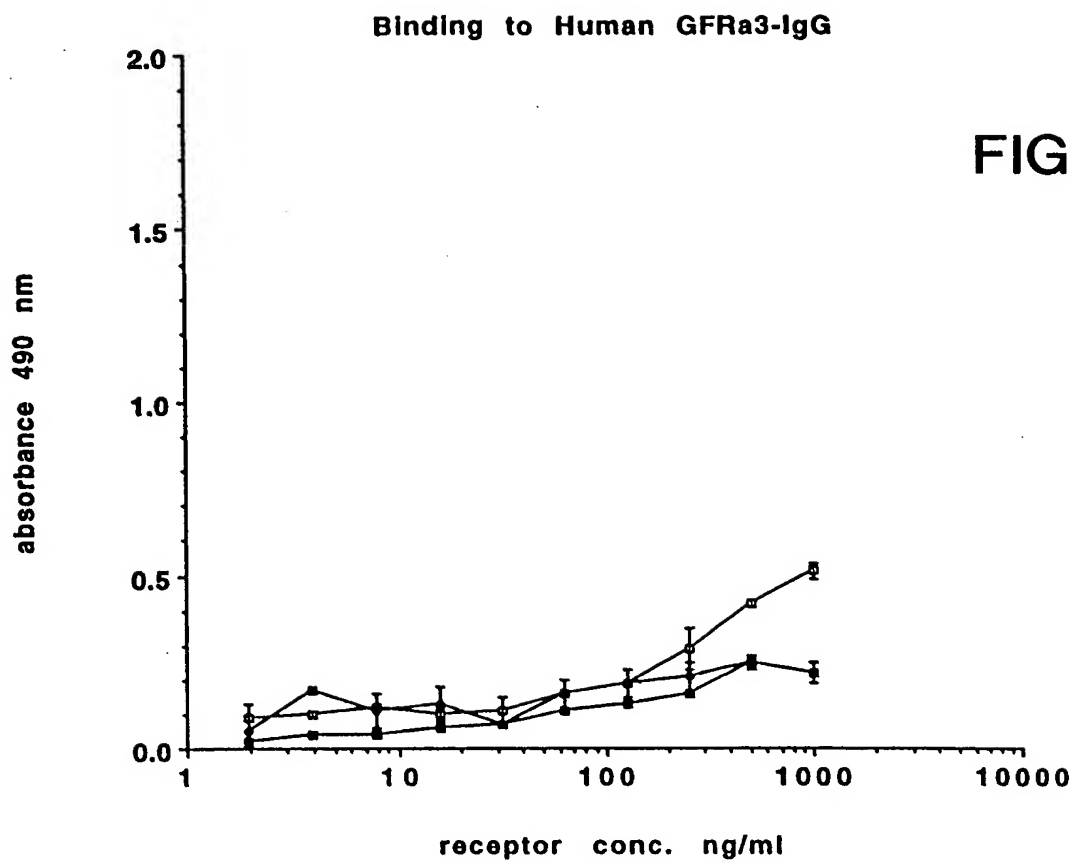


FIG. 10

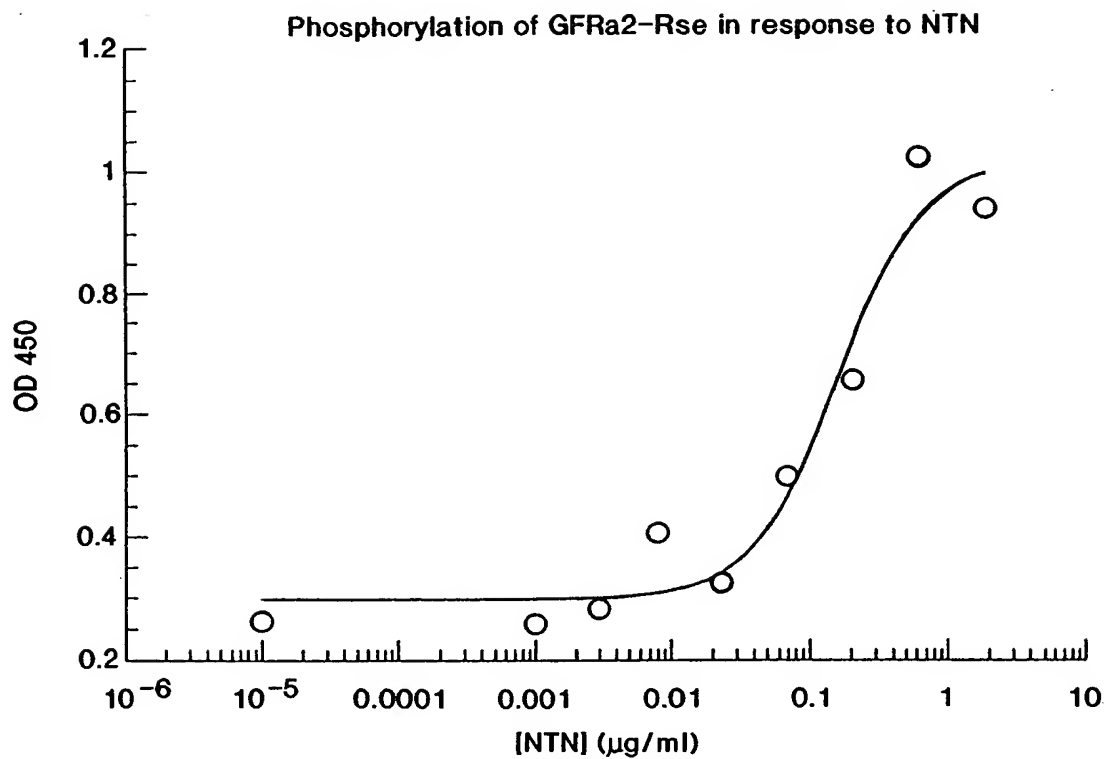


FIG. 11

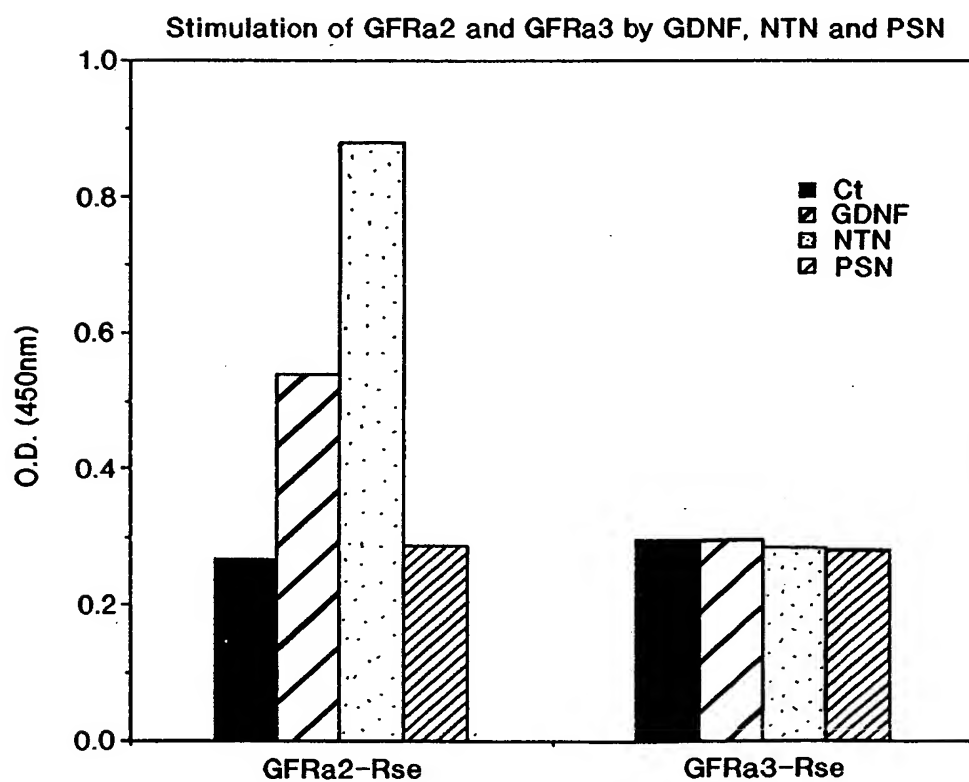


FIG. 12

Agonistic activity of anti gD mAbs in gD-alpha2-rse-KIRA

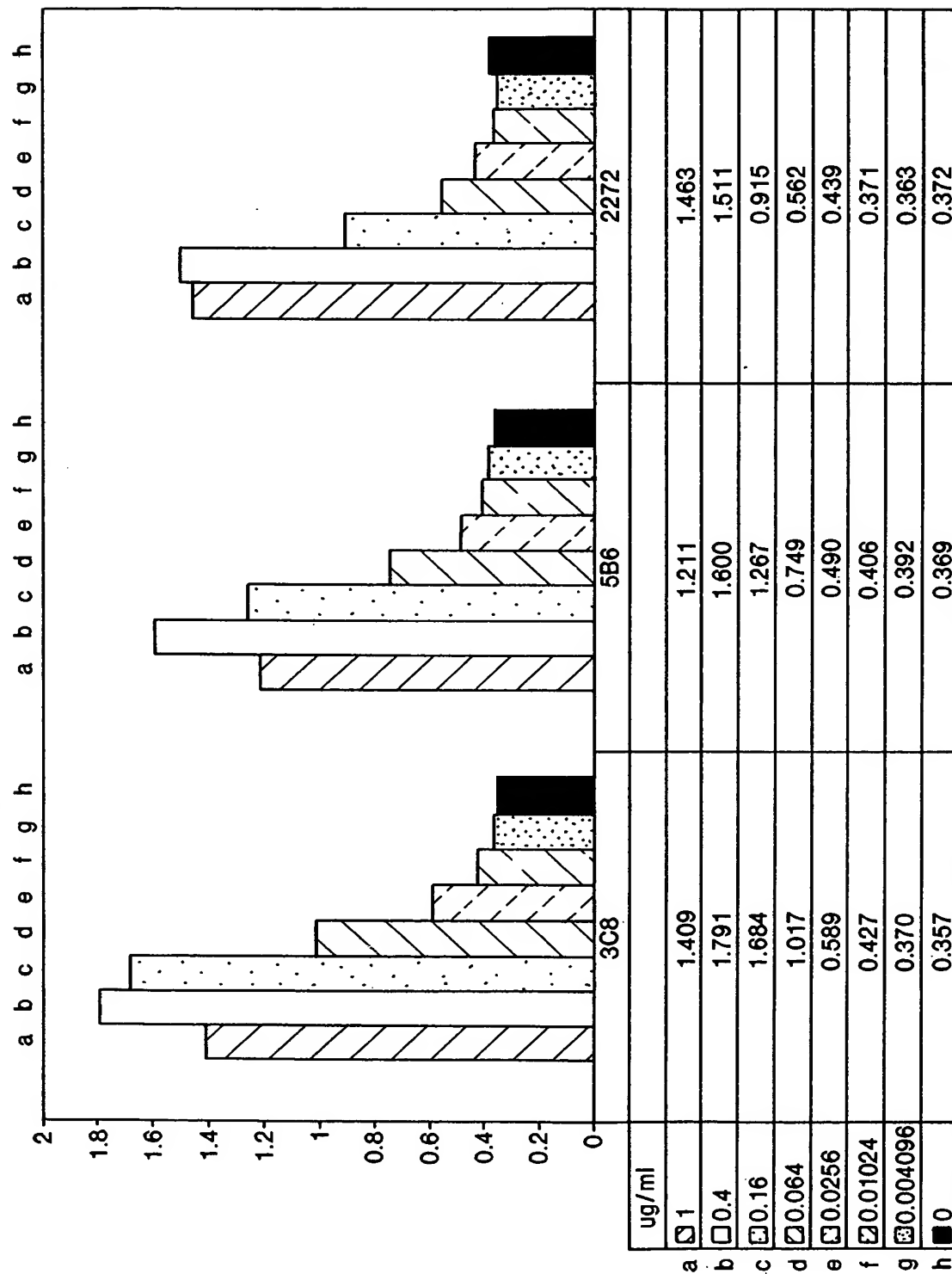


FIG. 13